MAIN SET OF CLAIMS

1. A genetic construct (10) which is suitable for the insertion/deletion and inversion for at least one target nucleotide sequence (A) and comprised of:

- a promoter/activator sequence (11) disposed upstream of a first and a second nucleotide sequence (1,2) encoding two different toxic molecules; and/or
- a first promoter/activator sequence (11) disposed upstream of a first nucleotide sequence (1) encoding a toxic molecule and disposed in the opposite direction, a second promoter/activator sequence (12) disposed upstream of a second nucleotide sequence encoding an antidote (2') to a second toxic molecule different from said first toxic molecule, and/or
- a promoter/activator sequence (11) disposed upstream a first nucleotide sequence (1) encoding a first toxic molecule and a second nucleotide sequence (2') encoding an antidote to a second toxic molecule different from said first toxic molecule.

2. The genetic construct (10) according to claim 1 suitable for the inversion of at least one target nucleotide sequence (A) and comprised of

- a first promoter/activator sequence (11) disposed upstream, a first nucleotide sequence (1) encoding a toxic molecule and a second nucleotide sequence (2') encoding an antidote to a second toxic molecule different from said first toxic molecule and,
- disposed in the opposite direction to the lecture orientation of the first promoter/activator sequence (11°).

3. The genetic construction according to the claim 2, wherein the third nucleotide sequence (1')

encoding an antidote to the first toxic molecule is under the control of a second promoter/activator sequence (12).

4. A nucleic acid construct according to claims 1 to 3, wherein each nucleotide sequence (1,2, 1',2') encoding a toxic molecule or an antidote to a toxic molecule is a nucleic sequence which encodes a fusion protein active as a toxic molecule or as an antidote to said toxic molecule, said fusion protein being made of a coding nucleotide sequence which comprises several unique cloning sites and a nucleotide sequence encoding a toxic molecule to a cell or an antidote to a toxic molecule.

5. The genetic construct (10) according to any of the preceding claims, which further comprises recombination sites disposed upstream and downstream the nucleotide sequence (s) (1, 2) encoding a toxic molecule and/or the nucleotide sequence (s) (1', 2') encoding an antidote to a toxic molecule.

6. The genetic construct (10) according to any of the preceding claims, wherein the sequences (1, 2, 1', 2') encoding toxic molecule and antidote to the toxic molecule are poison/antidote sequences.

7. The genetic construct according to the claim 6, wherein the poison/antidote sequences are selected from the group consisting of the following poison/antidote systems : CcdB/CcdA, Kid/Kis, Hok/Sok, Doc/Phd, RelE/RelB, PasA/PasB/PasC, MazE/MazF, ParE/ParD.

8. A cloning vector comprising at least one of the genetic construct (10) according to any of the preceding claims 1 to 7.

9. The vector according to claim 8 further comprising an origin of replication and a selectable marker, preferably an antibiotic resistance selectable marker.

10. A cell transformed by the genetic construct according to any of the preceding claims 1 to 7 or the vector according to any of the preceding claims 8 or 9 or comprising integrated in its chromosomal genome at least one genetic construct according to any of the preceding claims 1 to 7.

11. The cell according to claim 10 which is selected from the group consisting of prokaryote cells, plant cells, animal cells (including human cells) and fungi cells (including yeast cells).

12. A cloning and selection kit comprising one or more nucleic acid construct according to any of the preceding claims 1 to 7, one or more vectors according to claim 8 or 9 and cells to be transformed by said construct or vector, which are either resistant or sensitive to one or more of said toxic molecule (s), expressing one or more of said toxic molecule (s) or antidote (s) to said toxic molecule (s).

13. A method for an insertion and possibly a deletion and/or an inversion of a target nucleotide sequence (A) into a nucleic acid construct and comprising the following steps, preferably performed by an automate

- providing a nucleic acid construct according to any of the preceding claims 1 to 7, possibly integrated into the vector of the claim 8 or 9 or in the cell according to the claim 10 or 11 and obtaining the insertion of said target nucleotide sequence into the nucleic acid construct by inactivation of a nucleotide sequence encoding a toxic molecule and,
- selecting the nucleic acid construct having integrated said target nucleotide sequence in a cell which is sensible to said toxic molecule.

14. The method according to claim 12 which further comprises the steps of :

- possibly selecting said target nucleotide sequence from genome databases through analysis of said genomic sequence by the identification of exon-intron-structure and comparison with expression genetic databases,
- possibly providing primer sequences suitable for a genetic amplification and cloning of said target genetic sequence,
- possibly selecting elements of said nucleic acid construct presented in databases as well as cells to be transformed by said nucleic acid construct, and
- possibly providing the design of the nucleic acid construct suitable for the integration of said target nucleotide sequence and possibly recovering the design of the obtained virtual nucleic acid construct into a target memory database,

15. The method according to claim 13 or 14 which further comprises the step of the replacement of the target sequence by the elements that have been deleted following the insertion of said target sequence or by the integration of a target sequence having an inverted lecture orientation.

16. The method according to any of the preceding claims 13 to 15, wherein integration of the target sequence, replacement or inversion of the target sequence is obtained by classical restriction/ligation, site specific recombination, TOPO cloning and homologous recombination.

17. The method according to any of the preceding claims 13 to 16, which comprises the step of insertion/deletion and/or reversion of several target

nucleotide sequences (A, B, C, D, E, F) into multiple nucleic acid construct(s) and the step of selecting simultaneously the construct having integrated, deleted or inverted correctly said target sequences.

18. The method according to the claim 17, wherein the step of selecting simultaneously the construct having integrated, deleted or inverted correctly the target sequences is made in a single cell or in a single reaction tube.

19. Computer program comprising program codes means for performing the steps according to any of the preceding claims 13 to 18.

20. Computer program products comprising the program codes means on a computer readable medium for performing the steps of the method according to any of the preceding claims 13 to 18 when said program is run on a computer.

21. An automate connected to a database of a computer and which comprises the nucleic acid construct according to the claims 1 to 7 or the vector according to claims 8 or 9, or the cells according to the claims 10 to 11, or the elements of the kit according to the claim 12 and possibly the computer program of claim 19 or 20 for performing the method according to any of the preceding claims 13 to 18.